

Application No. 08/477,316  
Attorney's Docket No. 028723-060

wherein the chromosomal material is present in a morphologically identifiable cell nucleus; allowing said probe to bind to said targeted chromosomal material; and detecting said bound probe, wherein bound probe is indicative of the presence of target chromosomal material.

2 <sup>1</sup> <sub>2</sub> 48. (Three Times Amended) A method of staining targeted interphase chromosomal material based upon a nucleic acid segment employing a unique sequence high complexity nucleic acid probe of greater than about 40 kb, wherein said targeted chromosomal material is a genetic rearrangement associated with at least one chromosome in humans, said method comprising contacting said chromosomal material with a unique sequence high complexity nucleic acid probe of greater than about 40 kb, wherein the chromosomal material is present in a morphologically identifiable cell nucleus; allowing said probe to bind to said targeted chromosomal material; and detecting said bound probe, wherein bound probe is indicative of the presence of target chromosomal material.

3 <sup>1</sup> <sub>2</sub> 50. (Three Times Amended) A method of staining targeted interphase chromosomal material based upon a nucleic acid segment employing a unique sequence high complexity nucleic acid probe of greater than about 50,000 bases, wherein said targeted interphase chromosomal material is a genetic rearrangement associated with at least one chromosome in humans, said method comprising contacting said interphase chromosomal material with a unique sequence high complexity nucleic acid probe of greater than about 50,000 bases, wherein the chromosomal material is present in a morphologically identifiable cell nucleus; allowing said probe to bind to said targeted interphase chromosomal material; and detecting said bound probe, wherein bound probe is indicative of the presence of target interphase chromosomal material.

Application No. 08/477,316  
Attorney's Docket No. 028723-060

Please add the following new claims:

-- 12 59. The method of claim 48,<sup>2</sup> wherein complexity of the unique sequence high complexity nucleic acid probe is greater than about 100,000 bases.

<sup>F</sup> 13 60. The method of claim 50,<sup>3</sup> wherein complexity of the unique sequence high complexity nucleic acid probe is greater than about 100,000 bases. --